



RECEIVED
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TECH CENTER 1600/2900

1

SEQUENCE LISTING

<110> White, David
Zhou, Jianghong
Tartaglia, Louis A.

<120> LEPTIN INDUCED GENES

<130> 07334-109002

<140> US 09/804,357

<141> 2001-03-12

<150> US 09/195,896

<151> 1998-11-19

<150> US 09/150,857

<151> 1998-09-10

<140> US 60/106,379

<141> 1998-10-29

<160> 19

<170> FastSEQ for Windows Version 4.0

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caattcggga	gtcttggggc	cgagaaacca	acgtagggaa	ccagacagta	gtgagggtct	540
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<213> Mus musculus

<400> 2

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Gln Asp Lys Asn Gly Lys Gly Gly Val Ile Ile Pro Lys Glu Lys Phe
      35          40          45
Trp Lys Pro Pro Ser Thr Pro Arg Ala Tyr Trp Asn Arg Glu Gln Glu
      50          55          60
Lys Leu Asn Arg Trp Tyr Asn Pro Ile Leu Asn Arg Val Ala Asn Gln
      65          70          75          80
Thr Gly Glu Leu Ala Thr Ser Pro Asn Thr Ser His Leu Ser Tyr Cys
      85          90          95
Glu Pro Asp Ser Thr Val Met Thr Ala Val Thr Asp Phe Asn Asn Leu
      100          105          110
Pro Asp Arg Phe Lys Asp Phe Leu Leu Tyr Leu Arg Cys Arg Asn Tyr
      115          120          125
Ser Leu Leu Ile Asp Gln Pro Lys Lys Cys Ala Lys Lys Pro Phe Leu
      130          135          140
Leu Leu Ala Ile Lys Ser Leu Ile Pro His Phe Ala Arg Arg Gln Ala
      145          150          155          160
Ile Arg Glu Ser Trp Gly Arg Glu Thr Asn Val Gly Asn Gln Thr Val
      165          170          175
Val Arg Val Phe Leu Leu Gly Lys Thr Pro Pro Glu Asp Asn His Pro
      180          185          190
Asp Leu Ser Asp Met Leu Lys Phe Glu Ser Asp Lys His Gln Asp Ile
      195          200          205
Leu Met Trp Asn Tyr Arg Asp Thr Phe Phe Asn Leu Ser Leu Lys Glu
      210          215          220
Val Leu Phe Leu Arg Trp Val Ser Thr Ser Cys Pro Asp Ala Glu Phe
      225          230          235          240
Val Phe Lys Gly Asp Asp Val Phe Val Asn Thr His His Ile Leu
      245          250          255
Asn Tyr Leu Asn Ser Leu Ser Lys Ser Lys Ala Lys Asp Leu Phe Ile
      260          265          270
Gly Asp Val Ile His Asn Ala Gly Pro His Arg Asp Lys Lys Leu Lys
      275          280          285
Tyr Tyr Ile Pro Glu Val Phe Tyr Thr Gly Val Tyr Pro Pro Tyr Ala
      290          295          300
Gly Gly Gly Gly Phe Leu Tyr Ser Gly Pro Ala Leu Leu Arg Leu Tyr
      305          310          315          320
Ser Ala Thr Ser Arg Val His Leu Tyr Pro Ile Asp Asp Val Tyr Thr
      325          330          335
Gly Met Cys Leu Gln Lys Leu Gly Leu Val Pro Glu Lys His Lys Gly
      340          345          350
Phe Arg Thr Phe Asp Ile Glu Glu Lys Asn Lys Lys Asn Ile Cys Ser
      355          360          365
Tyr Ile Asp Leu Met Leu Val His Ser Arg Lys Pro Gln Glu Met Ile
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gtaataatcc cgaaagagaa gttctggaag ccacccagca ctcccggggc atactggaac      180
agggaacagg agaagctgaa caggtggtac aatcccatct tgaacagggt ggccaatcag      240
acaggggagc tagccacatc tccaaacaca agtcacctga gctattgtga accagactcg      300
acggtcatga cagctgtgac agattttaat aatctgccgg acagatttaa agactttctc      360
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aagcccttct tactattggc gataaagtcc ctcatccac attttgccag aaggcaagca      480
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ctgttgggca agacaccccc agaggacaac caccctgacc tttcggacat gcttaagttt      600
gagagtgaca agcaccagga catcctcatg tggaaactata gagacacatt cttcaacctg      660
tccctgaagg aagtgtgttt tcttaggtgg gtgagcactt cctgtccaga cgcagagttt      720
gtcttcaagg gcgatgatga cgtgtttgtg aacacccatc acatccttaa ttacttgaat      780
agcttatcca agagcaaagc caaagacttg ttcataggtg acgtgatcca caatgctggg      840
cctcaccggg ataagaaact gaagtactac atcccagaag tctctacac cggcgtctac      900
ccaccgtatg ccgggggtgg tggattcctg tactccggcc cccttgccct gaggctgtac      960
agtgcgacta gccgggtcca tctctaccct attgatgatg tttatacggg aatgtgcctt     1020
cagaaactgg gccttgttcc agagaagcac aaaggettca ggacatttga tattgaagag     1080
aaaaataaga aaaatatttg ttcctatata gacctaatgt tagtacatag cagaaaacct     1140
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<210> 4

<211> 365

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          20          25          30
Lys Leu Asn Arg Trp Tyr Asn Pro Ile Leu Asn Arg Val Ala Asn Gln
          35          40          45
Thr Gly Glu Leu Ala Thr Ser Pro Asn Thr Ser His Leu Ser Tyr Cys
          50          55          60
Glu Pro Asp Ser Thr Val Met Thr Ala Val Thr Asp Phe Asn Asn Leu
          65          70          75          80
Pro Asp Arg Phe Lys Asp Phe Leu Leu Tyr Leu Arg Cys Arg Asn Tyr
          85          90          95
Ser Leu Leu Ile Asp Gln Pro Lys Lys Cys Ala Lys Lys Pro Phe Leu
          100          105          110
Leu Leu Ala Ile Lys Ser Leu Ile Pro His Phe Ala Arg Arg Gln Ala
          115          120          125
Ile Arg Glu Ser Trp Gly Arg Glu Thr Asn Val Gly Asn Gln Thr Val
          130          135          140
Val Arg Val Phe Leu Leu Gly Lys Thr Pro Pro Glu Asp Asn His Pro
          145          150          155          160
Asp Leu Ser Asp Met Leu Lys Phe Glu Ser Asp Lys His Gln Asp Ile
          165          170          175
Leu Met Trp Asn Tyr Arg Asp Thr Phe Phe Asn Leu Ser Leu Lys Glu
          180          185          190
Val Leu Phe Leu Arg Trp Val Ser Thr Ser Cys Pro Asp Ala Glu Phe
          195          200          205

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Val Phe Lys Gly Asp Asp Asp Val Phe Val Asn Thr His His Ile Leu
 210 215 220
 Asn Tyr Leu Asn Ser Leu Ser Lys Ser Lys Ala Lys Asp Leu Phe Ile
 225 230 235 240
 Gly Asp Val Ile His Asn Ala Gly Pro His Arg Asp Lys Lys Leu Lys
 245 250 255
 Tyr Tyr Ile Pro Glu Val Phe Tyr Thr Gly Val Tyr Pro Pro Tyr Ala
 260 265 270
 Gly Gly Gly Gly Phe Leu Tyr Ser Gly Pro Ala Leu Leu Arg Leu Tyr
 275 280 285
 Ser Ala Thr Ser Arg Val His Leu Tyr Pro Ile Asp Asp Val Tyr Thr
 290 295 300
 Gly Met Cys Leu Gln Lys Leu Gly Leu Val Pro Glu Lys His Lys Gly
 305 310 315 320
 Phe Arg Thr Phe Asp Ile Glu Glu Lys Asn Lys Lys Asn Ile Cys Ser
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<212> DNA

<213> Mus musculus

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tacaaacacc	ccaatatacc	caatgtggtt	ttttgggacc	tgccctgggat	tggaagcaca	360
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60
120

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<210> 8

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<212> PRT

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Thr Gly Ser Lys Pro Phe Ser His Leu Thr Val Ala Arg Lys Asn Phe
          35             40             45
Thr Phe Gly Asn Ile Arg Thr Arg Pro Ile Asn Pro His Ser Phe Glu
          50             55             60
Phe Leu Ile Asn Glu Pro Asn Lys Cys Glu Lys Asn Ile Pro Phe Leu
          65             70             75             80
Val Ile Leu Ile Ser Thr Thr His Lys Glu Phe Asp Ala Arg Gln Ala
          85             90             95
Ile Arg Glu Thr Trp Gly Asp Glu Asn Asn Phe Lys Gly Ile Lys Ile
          100            105            110
Ala Thr Leu Phe Leu Leu Gly Lys Asn Ala Asp Pro Val Leu Asn Gln
          115            120            125
Met Val Glu Gln Glu Ser Gln Ile Phe His Asp Ile Ile Val Glu Asp
          130            135            140
Phe Ile Asp Ser Tyr His Asn Leu Thr Leu Lys Thr Leu Met Gly Met
          145            150            155            160
Arg Trp Val Ala Thr Phe Cys Ser Lys Ala Lys Tyr Val Met Lys Thr
          165            170            175
Asp Ser Asp Ile Phe Val Asn Met Asp Asn Leu Ile Tyr Lys Leu Leu
          180            185            190
Lys Pro Ser Thr Lys Pro Arg Arg Arg Tyr Phe Thr Gly Tyr Val Ile
          195            200            205
Asn Gly Gly Pro Ile Arg Asp Val Arg Ser Lys Trp Tyr Met Pro Arg
          210            215            220
Asp Leu Tyr Pro Asp Ser Asn Tyr Pro Pro Phe Cys Ser Gly Thr Gly
          225            230            235            240
Tyr Ile Phe Ser Ala Asp Val Ala Glu Leu Ile Tyr Lys Thr Ser Leu
          245            250            255

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Arg	Lys	Leu	Gly	Ile	His	Pro	Phe	Gln	Asn	Ser	Gly	Phe	Asn	His	Trp
		275					280					285			
Lys	Met	Ala	Tyr	Ser	Leu	Cys	Arg	Tyr	Arg	Arg	Val	Ile	Thr	Val	His
	290					295					300				
Gln	Ile	Ser	Pro	Glu	Glu	Met	His	Arg	Ile	Trp	Asn	Asp	Met	Ser	Ser
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<211> 331

<212> PRT

<213> Mus musculus

<400> 9

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			20					25					30		
Ile	Trp	Tyr	Leu	Ser	Leu	Pro	His	Tyr	Asn	Val	Ile	Glu	Arg	Val	Asn
		35					40					45			
Trp	Met	Tyr	Phe	Tyr	Glu	Tyr	Glu	Pro	Ile	Tyr	Arg	Gln	Asp	Phe	Arg
	50					55					60				
Phe	Thr	Leu	Arg	Glu	His	Ser	Asn	Cys	Ser	His	Gln	Asn	Pro	Phe	Leu
65					70					75					80
Val	Ile	Leu	Val	Thr	Ser	Arg	Pro	Ser	Asp	Val	Lys	Ala	Arg	Gln	Ala
				85					90					95	
Ile	Arg	Val	Thr	Trp	Gly	Glu	Lys	Lys	Ser	Trp	Trp	Gly	Tyr	Glu	Val
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Leu	Thr	Phe	Phe	Leu	Leu	Gly	Gln	Gln	Ala	Glu	Arg	Glu	Asp	Lys	Thr
	115					120						125			
Leu	Ala	Leu	Ser	Leu	Glu	Asp	Glu	His	Val	Leu	Tyr	Gly	Asp	Ile	Ile
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Met	Ala	Phe	Arg	Trp	Val	Met	Glu	Phe	Cys	Pro	Asn	Ala	Lys	Tyr	Ile
				165					170					175	
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Tyr	Leu	Leu	Asn	Leu	Asn	His	Ser	Glu	Lys	Phe	Phe	Thr	Gly	Tyr	Pro
	195					200						205			
Leu	Ile	Asp	Asn	Tyr	Ser	Tyr	Arg	Gly	Phe	Phe	His	Lys	Asn	His	Ile
	210					215					220				
Ser	Tyr	Gln	Glu	Tyr	Pro	Phe	Lys	Val	Phe	Pro	Pro	Tyr	Cys	Ser	Gly
225					230					235					240
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		260						265					270		
Cys	Leu	Asn	Leu	Leu	Lys	Val	Asp	Ile	His	Ile	Pro	Glu	Asp	Thr	Asn
	275						280						285		
Leu	Phe	Phe	Leu	Tyr	Arg	Ile	His	Leu	Asp	Val	Cys	Gln	Leu	Arg	Arg
	290					295					300				
Val	Ile	Ala	Ala	His	Gly	Phe	Ser	Ser	Lys	Glu	Ile	Ile	Thr	Phe	Trp
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<210> 10
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 <213> *Drosophilea melonogaster*

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 35 40 45
 Gly Ser Gly Ser Ala Ser Ser Gly Leu Asp Lys Phe Ala Tyr Leu Arg
 50 55 60
 Val Pro Ser Phe Thr Ala Glu Val Pro Val Asp Gln Pro Ala Arg Leu
 65 70 75 80
 Thr Met Leu Ile Lys Ser Ala Val Gly Asn Ser Arg Arg Arg Glu Ala
 85 90 95
 Ile Arg Arg Thr Trp Gly Tyr Glu Gly Arg Phe Ser Asp Val His Leu
 100 105 110
 Arg Arg Val Phe Leu Leu Gly Thr Ala Glu Asp Ser Glu Lys Asp Val
 115 120 125
 Ala Trp Glu Ser Arg Glu His Gly Asp Ile Leu Gln Ala Asp Phe Thr
 130 135 140
 Asp Ala Tyr Phe Asn Asn Thr Leu Lys Thr Met Leu Gly Met Arg Trp
 145 150 155 160
 Ala Ser Glu Gln Phe Asn Arg Ser Glu Phe Tyr Leu Phe Val Asp Asp
 165 170 175
 Asp Tyr Tyr Val Ser Ala Lys Asn Val Leu Lys Phe Leu Gly Arg Gly
 180 185 190
 Arg Gln Ser His Gln Pro Glu Leu Leu Phe Ala Gly His Val Phe Gln
 195 200 205
 Thr Ser Pro Leu Arg His Lys Phe Ser Lys Trp Tyr Val Ser Leu Glu
 210 215 220
 Glu Tyr Pro Phe Asp Arg Trp Pro Pro Tyr Val Thr Ala Gly Ala Phe
 225 230 235 240
 Ile Leu Ser Gln Lys Ala Leu Arg Gln Leu Tyr Ala Ala Ser Val His
 245 250 255
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 260 265 270
 Lys Ala Gly Ile Ser Leu Gln His Cys Asp Asp Phe Arg Phe His Arg
 275 280 285
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<210> 11
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 <213> *Homo sapien*

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Leu 35	Val 36	Phe 37	Leu 38	Phe 39	Ala 40	Met 41	Phe 42	Leu 43	Phe 44	Phe 45	Asn 46	His 47	His 48	Asp 49	Trp 50
Leu 50	Pro 51	Gly 52	Arg 53	Ala 54	Gly 55	Phe 56	Lys 57	Glu 58	Asn 59	Pro 60	Val 61	Thr 62	Tyr 63	Thr 64	Phe 65
Arg 65	Gly 66	Phe 67	Arg 68	Ser 69	Thr 70	Lys 71	Ser 72	Glu 73	Thr 74	Asn 75	His 76	Ser 77	Ser 78	Leu 79	Arg 80
Asn 85	Ile 86	Trp 87	Lys 88	Glu 89	Thr 90	Val 91	Pro 92	Gln 93	Thr 94	Leu 95	Arg 96	Pro 97	Gln 98	Thr 99	Ala 100
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Pro 175	Gly 176	Gln 177	Ile 178	Glu 179	Ala 180	Arg 181	Arg 182	Ala 183	Ile 184	Arg 185	Gln 186	Thr 187	Trp 188	Gly 189	Asn 190
Glu 195	Ser 196	Leu 197	Ala 198	Pro 199	Gly 200	Ile 201	Gln 202	Ile 203	Thr 204	Arg 205	Ile 206	Phe 207	Leu 208	Leu 209	Gly 210
Leu 215	Ser 216	Ile 217	Lys 218	Leu 219	Asn 220	Gly 221	Tyr 222	Leu 223	Gln 224	Arg 225	Ala 226	Ile 227	Leu 228	Glu 229	Glu 230
Ser 235	Arg 236	Gln 237	Tyr 238	His 239	Asp 240	Ile 241	Ile 242	Gln 243	Gln 244	Glu 245	Tyr 246	Leu 247	Asp 248	Thr 249	Tyr 250
Tyr 255	Asn 256	Leu 257	Thr 258	Ile 259	Lys 260	Thr 261	Leu 262	Met 263	Gly 264	Met 265	Asn 266	Trp 267	Val 268	Ala 269	Thr 270
Tyr 275	Cys 276	Pro 277	His 278	Ile 279	Pro 280	Tyr 281	Val 282	Met 283	Lys 284	Thr 285	Asp 286	Ser 287	Asp 288	Met 289	Phe 290
Val 295	Asn 296	Thr 297	Glu 298	Tyr 299	Leu 300	Ile 301	Asn 302	Lys 303	Leu 304	Leu 305	Lys 306	Pro 307	Asp 308	Leu 309	Pro 310
Pro 315	Arg 316	His 317	Asn 318	Tyr 319	Phe 320	Thr 321	Gly 322	Tyr 323	Leu 324	Met 325	Arg 326	Gly 327	Tyr 328	Ala 329	Pro 330
Asn 335	Arg 336	Asn 337	Lys 338	Asp 339	Ser 340	Lys 341	Trp 342	Tyr 343	Met 344	Pro 345	Pro 346	Asp 347	Leu 348	Tyr 349	Pro 350
Ser 355	Glu 356	Arg 357	Tyr 358	Pro 359	Val 360	Phe 361	Cys 362	Ser 363	Gly 364	Thr 365	Gly 366	Tyr 367	Val 368	Phe 369	Ser 370
Gly 375	Asp 376	Leu 377	Ala 378	Glu 379	Lys 380	Ile 381	Phe 382	Lys 383	Val 384	Ser 385	Leu 386	Gly 387	Ile 388	Arg 389	Arg 390
Leu 395	His 396	Leu 397	Glu 398	Asp 399	Val 400	Tyr 401	Val 402	Gly 403	Ile 404	Cys 405	Leu 406	Ala 407	Lys 408	Leu 409	Arg 410
Ile 415	Asp 416	Pro 417	Val 418	Pro 419	Pro 420	Pro 421	Asn 422	Glu 423	Phe 424	Val 425	Phe 426	Asn 427	His 428	Trp 429	Arg 430
Val 435	Ser 436	Tyr 437	Ser 438	Ser 439	Cys 440	Lys 441	Tyr 442	Ser 443	His 444	Leu 445	Ile 446	Thr 447	Ser 448	His 449	Gln 450
Phe 455	Gln 456	Pro 457	Ser 458	Glu 459	Leu 460	Ile 461	Lys 462	Tyr 463	Trp 464	Asn 465	His 466	Leu 467	Gln 468	Gln 469	Asn 470

<210> 12
 <211> 229
 <212> PRT
 <213> Artificial sequence

<220>
 <221> VARIANT
 <222> (1)...(229)
 <223> Xaa = Any Amino Acid

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 1 5 10 15
 Val Xaa Leu Xaa Xaa Xaa Phe Xaa Phe Leu Xaa His Trp Phe Phe Pro
 20 25 30
 Ile Trp Tyr Leu Ser Ile Pro Leu Arg Pro Gln Thr Gly Ser Xaa Ser
 35 40 45
 Xaa Ser Xaa Xaa Leu Ser His Leu Tyr Asn Thr Val Xaa Arg Xaa Asn
 50 55 60
 Xaa Xaa Phe Asn Asn Xaa Xaa Thr Arg Pro Ile Asn Ser Xaa Xaa Phe
 65 70 75 80
 Glu Phe Leu Ile Asp Glu Pro Xaa Lys Cys Xaa Lys Lys Pro Phe Leu
 85 90 95
 Val Leu Leu Ile Lys Ser Xaa Pro Gly Xaa Phe Xaa Ala Arg Gln Ala
 100 105 110
 Ile Arg Glu Thr Trp Gly Xaa Glu Xaa Asn Phe Xaa Gly Ile Xaa Val
 115 120 125
 Xaa Arg Val Phe Leu Leu Gly Lys Xaa Ala Glu Xaa Xaa Asp Pro Xaa
 130 135 140
 Leu Xaa Xaa Met Val Glu Xaa Glu Ser Arg Xaa His Gly Asp Ile Ile
 145 150 155 160
 Gln Gln Asp Phe Leu Asp Thr Tyr Phe Asn Leu Thr Leu Lys Thr Leu
 165 170 175
 Met Gly Met Arg Trp Val Ala Thr Phe Cys Pro Xaa Ala Glu Tyr Val
 180 185 190
 Met Lys Thr Asp Ser Asp Val Phe Val Asn Thr Xaa Asn Leu Leu Asn
 195 200 205
 Lys Leu Leu Lys Pro Ser Leu Ser His Arg Xaa Xaa Leu Phe Thr Gly
 210 215 220
 Tyr Val Ile Xaa Gly
 225

<210> 13
 <211> 1707
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
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<221> misc_feature
 <222> (1)...(1707)
 <223> n = A,T,C or G

<400> 13

acgcgtccgc gcagcggcag cggcagcagc ggcaacaagt gccggaggct agcagagcca	60
agccggagca gtccctgccg ccgacaccgc cgggccgccc gtccggggcg ccgcgcattg	120
agcgtgagct gcggcggtcg ccgggctgag ccgcgcggag cggccgggac gtggatgtgg	180
ccgcgatctc ccgcccttgc ccccgccccg ccgagctgga gctgctcccg gacaagatat	240
gagaa atg agt gtt gga cgt cga aga ata aag ttg ttg ggt atc ctg atg	290
Met Ser Val Gly Arg Arg Arg Ile Lys Leu Leu Gly Ile Leu Met	
1 5 10 15	
atg gca aat gtc ttc att tat ttt att atg gaa gtc tcc aaa agc agt	338
Met Ala Asn Val Phe Ile Tyr Phe Ile Met Glu Val Ser Lys Ser Ser	
20 25 30	
agc caa gaa aaa aat gga aaa ggg gaa gta ata ata ccc aaa gag aag	386
Ser Gln Glu Lys Asn Gly Lys Gly Glu Val Ile Ile Pro Lys Glu Lys	
35 40 45	
ttc tgg aag ata tct acc cct ccc gag gca tac tgg aac cga gag caa	434
Phe Trp Lys Ile Ser Thr Pro Pro Glu Ala Tyr Trp Asn Arg Glu Gln	
50 55 60	
gag aag ctg aac cgg cag tac aac ccc atc ctg agc atg ctg acc aac	482
Glu Lys Leu Asn Arg Gln Tyr Asn Pro Ile Leu Ser Met Leu Thr Asn	
65 70 75	
cag acg ggg gag gcg ggc agg ctc tcc aat ata agc cat ctg aac tac	530
Gln Thr Gly Glu Ala Gly Arg Leu Ser Asn Ile Ser His Leu Asn Tyr	
80 85 90 95	
tgc gaa cct gac ctg agg gtc acg tcg gtg gtt acg ggt ttt aac aac	578
Cys Glu Pro Asp Leu Arg Val Thr Ser Val Val Thr Gly Phe Asn Asn	
100 105 110	
ttg ccg gac aga ttt aaa gac ttt ctg ctg tat ttg aga tgc cgc aat	626
Leu Pro Asp Arg Phe Lys Asp Phe Leu Leu Tyr Leu Arg Cys Arg Asn	
115 120 125	
tat tca ctg ctt ata gat cag ccg gat aag tgt gca aag aaa cct ttc	674
Tyr Ser Leu Leu Ile Asp Gln Pro Asp Lys Cys Ala Lys Lys Pro Phe	
130 135 140	
ttg ttg ctg gcg att aag tcc ctc act cca cat ttt gcc aga agg caa	722
Leu Leu Leu Ala Ile Lys Ser Leu Thr Pro His Phe Ala Arg Arg Gln	
145 150 155	
gca atc cgg gaa tcc tgg ggc caa gaa agc aac gca ggg aac caa acg	770
Ala Ile Arg Glu Ser Trp Gly Gln Glu Ser Asn Ala Gly Asn Gln Thr	
160 165 170 175	
gtg gtg cga gtc ttc ctg ctg ggc cag aca ccc cca gag gac aac cac	818
Val Val Arg Val Phe Leu Leu Gly Gln Thr Pro Pro Glu Asp Asn His	
180 185 190	
ccc gac ctt tca gat atg ctg aaa ttt gag agt gag aag cac caa gac	866
Pro Asp Leu Ser Asp Met Leu Lys Phe Glu Ser Glu Lys His Gln Asp	
195 200 205	

att ctt atg tgg aac tac aga gac act ttc ttc aac ttg tct ctg aag 914
 Ile Leu Met Trp Asn Tyr Arg Asp Thr Phe Phe Asn Leu Ser Leu Lys
 210 215 220

gaa gtg ctg ttt ctc agg tgg gta agt act tcc tgc cca gac act gag 962
 Glu Val Leu Phe Leu Arg Trp Val Ser Thr Ser Cys Pro Asp Thr Glu
 225 230 235

ttt gtt ttc aag ggc gat gac gat gtt ttt gtg aac acc cat cac atc 1010
 Phe Val Phe Lys Gly Asp Asp Asp Val Phe Val Asn Thr His His Ile
 240 245 250 255

ctg aat tac ttg aat agt tta tcc aag acc aaa gcc aaa gat ctc ttc 1058
 Leu Asn Tyr Leu Asn Ser Leu Ser Lys Thr Lys Ala Lys Asp Leu Phe
 260 265 270

ata ggt gat gtg atc cac aat gct gga cct cat cgg gat aag aag ctg 1106
 Ile Gly Asp Val Ile His Asn Ala Gly Pro His Arg Asp Lys Lys Leu
 275 280 285

aag tac tac atc cca gaa gtt gtt tac tct ggc ctc tac cca ccc tat 1154
 Lys Tyr Tyr Ile Pro Glu Val Val Tyr Ser Gly Leu Tyr Pro Pro Tyr
 290 295 300

gca ggg gga ggg ggg ttc ctc tac tcc ggc cac ctg gcc ctg agg ctg 1202
 Ala Gly Gly Gly Gly Phe Leu Tyr Ser Gly His Leu Ala Leu Arg Leu
 305 310 315

tac cat atc act gac cag gtc cat ctc tac ccc att gat gac gtt tat 1250
 Tyr His Ile Thr Asp Gln Val His Leu Tyr Pro Ile Asp Asp Val Tyr
 320 325 330 335

act gga atg tgc ctt cag aaa ctc ggc ctc gtt cca gag aaa cac aaa 1298
 Thr Gly Met Cys Leu Gln Lys Leu Gly Leu Val Pro Glu Lys His Lys
 340 345 350

ggc ttc agg aca ttt gat atc gag gag aaa aac aaa aat aac atc tgc 1346
 Gly Phe Arg Thr Phe Asp Ile Glu Glu Lys Asn Lys Asn Asn Ile Cys
 355 360 365

tcc tat gta gat ctg atg tta gta cat agt aga aaa cct caa gag atg 1394
 Ser Tyr Val Asp Leu Met Leu Val His Ser Arg Lys Pro Gln Glu Met
 370 375 380

att gat att tgg tct cag ttg cag agt gct cat tta aaa tgc 1436
 Ile Asp Ile Trp Ser Gln Leu Gln Ser Ala His Leu Lys Cys
 385 390 395

taaaatagat acaaaactcaa tttkgsatwg raaggggtwt tttgratwgg ycccatgttg 1496
 ggggtctcaca ttagagtaat ttctatttina ancatgaaat tgccttttatg agtgataccc 1556
 atttanggcc tctaancctt catttgnact cacgtgaaga agggaaagcg ggagaaggta 1616
 atttntttat ggtgaatggc aggatatttg tctgacttac cgntagggga ntttaaaact 1676
 ggnccctttt gaatctgttt ggatggccct t 1707

<210> 14

<211> 397

<212> PRT
 <213> Homo sapiens

<400> 14

Met	Ser	Val	Gly	Arg	Arg	Arg	Ile	Lys	Leu	Leu	Gly	Ile	Leu	Met	Met
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Ala	Asn	Val	Phe	Ile	Tyr	Phe	Ile	Met	Glu	Val	Ser	Lys	Ser	Ser	Ser
		20						25					30		
Gln	Glu	Lys	Asn	Gly	Lys	Gly	Glu	Val	Ile	Ile	Pro	Lys	Glu	Lys	Phe
		35					40					45			
Trp	Lys	Ile	Ser	Thr	Pro	Pro	Glu	Ala	Tyr	Trp	Asn	Arg	Glu	Gln	Glu
		50				55					60				
Lys	Leu	Asn	Arg	Gln	Tyr	Asn	Pro	Ile	Leu	Ser	Met	Leu	Thr	Asn	Gln
		65			70					75					80
Thr	Gly	Glu	Ala	Gly	Arg	Leu	Ser	Asn	Ile	Ser	His	Leu	Asn	Tyr	Cys
				85					90					95	
Glu	Pro	Asp	Leu	Arg	Val	Thr	Ser	Val	Val	Thr	Gly	Phe	Asn	Asn	Leu
			100					105					110		
Pro	Asp	Arg	Phe	Lys	Asp	Phe	Leu	Leu	Tyr	Leu	Arg	Cys	Arg	Asn	Tyr
		115					120					125			
Ser	Leu	Leu	Ile	Asp	Gln	Pro	Asp	Lys	Cys	Ala	Lys	Lys	Pro	Phe	Leu
		130				135						140			
Leu	Leu	Ala	Ile	Lys	Ser	Leu	Thr	Pro	His	Phe	Ala	Arg	Arg	Gln	Ala
					150					155					160
Ile	Arg	Glu	Ser	Trp	Gly	Gln	Glu	Ser	Asn	Ala	Gly	Asn	Gln	Thr	Val
				165					170					175	
Val	Arg	Val	Phe	Leu	Leu	Gly	Gln	Thr	Pro	Pro	Glu	Asp	Asn	His	Pro
			180					185					190		
Asp	Leu	Ser	Asp	Met	Leu	Lys	Phe	Glu	Ser	Glu	Lys	His	Gln	Asp	Ile
		195					200					205			
Leu	Met	Trp	Asn	Tyr	Arg	Asp	Thr	Phe	Phe	Asn	Leu	Ser	Leu	Lys	Glu
		210				215					220				
Val	Leu	Phe	Leu	Arg	Trp	Val	Ser	Thr	Ser	Cys	Pro	Asp	Thr	Glu	Phe
					230					235					240
Val	Phe	Lys	Gly	Asp	Asp	Val	Phe	Val	Asn	Thr	His	His	Ile	Leu	
				245					250				255		
Asn	Tyr	Leu	Asn	Ser	Leu	Ser	Lys	Thr	Lys	Ala	Lys	Asp	Leu	Phe	Ile
			260					265					270		
Gly	Asp	Val	Ile	His	Asn	Ala	Gly	Pro	His	Arg	Asp	Lys	Lys	Leu	Lys
		275					280					285			
Tyr	Tyr	Ile	Pro	Glu	Val	Val	Tyr	Ser	Gly	Leu	Tyr	Pro	Pro	Tyr	Ala
		290				295						300			
Gly	Gly	Gly	Gly	Phe	Leu	Tyr	Ser	Gly	His	Leu	Ala	Leu	Arg	Leu	Tyr
					310					315					320
His	Ile	Thr	Asp	Gln	Val	His	Leu	Tyr	Pro	Ile	Asp	Asp	Val	Tyr	Thr
				325					330					335	
Gly	Met	Cys	Leu	Gln	Lys	Leu	Gly	Leu	Val	Pro	Glu	Lys	His	Lys	Gly
			340					345					350		
Phe	Arg	Thr	Phe	Asp	Ile	Glu	Glu	Lys	Asn	Lys	Asn	Asn	Ile	Cys	Ser
			355				360						365		
Tyr	Val	Asp	Leu	Met	Leu	Val	His	Ser	Arg	Lys	Pro	Gln	Glu	Met	Ile
		370				375					380				
Asp	Ile	Trp	Ser	Gln	Leu	Gln	Ser	Ala	His	Leu	Lys	Cys			
					385		390				395				

<210> 15
 <211> 365

<212> PRT

<213> Homo sapiens

<400> 15

Gln	Glu	Lys	Asn	Gly	Lys	Gly	Glu	Val	Ile	Ile	Pro	Lys	Glu	Lys	Phe	1	5	10	15
Trp	Lys	Ile	Ser	Thr	Pro	Pro	Glu	Ala	Tyr	Trp	Asn	Arg	Glu	Gln	Glu	20	25	30	
Lys	Leu	Asn	Arg	Gln	Tyr	Asn	Pro	Ile	Leu	Ser	Met	Leu	Thr	Asn	Gln	35	40	45	
Thr	Gly	Glu	Ala	Gly	Arg	Leu	Ser	Asn	Ile	Ser	His	Leu	Asn	Tyr	Cys	50	55	60	
Glu	Pro	Asp	Leu	Arg	Val	Thr	Ser	Val	Val	Thr	Gly	Phe	Asn	Asn	Leu	65	70	75	80
Pro	Asp	Arg	Phe	Lys	Asp	Phe	Leu	Leu	Tyr	Leu	Arg	Cys	Arg	Asn	Tyr	85	90	95	
Ser	Leu	Leu	Ile	Asp	Gln	Pro	Asp	Lys	Cys	Ala	Lys	Lys	Pro	Phe	Leu	100	105	110	
Leu	Leu	Ala	Ile	Lys	Ser	Leu	Thr	Pro	His	Phe	Ala	Arg	Arg	Gln	Ala	115	120	125	
Ile	Arg	Glu	Ser	Trp	Gly	Gln	Glu	Ser	Asn	Ala	Gly	Asn	Gln	Thr	Val	130	135	140	
Val	Arg	Val	Phe	Leu	Leu	Gly	Gln	Thr	Pro	Pro	Glu	Asp	Asn	His	Pro	145	150	155	160
Asp	Leu	Ser	Asp	Met	Leu	Lys	Phe	Glu	Ser	Glu	Lys	His	Gln	Asp	Ile	165	170	175	
Leu	Met	Trp	Asn	Tyr	Arg	Asp	Thr	Phe	Phe	Asn	Leu	Ser	Leu	Lys	Glu	180	185	190	
Val	Leu	Phe	Leu	Arg	Trp	Val	Ser	Thr	Ser	Cys	Pro	Asp	Thr	Glu	Phe	195	200	205	
Val	Phe	Lys	Gly	Asp	Asp	Asp	Val	Phe	Val	Asn	Thr	His	His	Ile	Leu	210	215	220	
Asn	Tyr	Leu	Asn	Ser	Leu	Ser	Lys	Thr	Lys	Ala	Lys	Asp	Leu	Phe	Ile	225	230	235	240
Gly	Asp	Val	Ile	His	Asn	Ala	Gly	Pro	His	Arg	Asp	Lys	Lys	Leu	Lys	245	250	255	
Tyr	Tyr	Ile	Pro	Glu	Val	Val	Tyr	Ser	Gly	Leu	Tyr	Pro	Pro	Tyr	Ala	260	265	270	
Gly	Gly	Gly	Gly	Phe	Leu	Tyr	Ser	Gly	His	Leu	Ala	Leu	Arg	Leu	Tyr	275	280	285	
His	Ile	Thr	Asp	Gln	Val	His	Leu	Tyr	Pro	Ile	Asp	Asp	Val	Tyr	Thr	290	295	300	
Gly	Met	Cys	Leu	Gln	Lys	Leu	Gly	Leu	Val	Pro	Glu	Lys	His	Lys	Gly	305	310	315	320
Phe	Arg	Thr	Phe	Asp	Ile	Glu	Glu	Lys	Asn	Lys	Asn	Asn	Ile	Cys	Ser	325	330	335	
Tyr	Val	Asp	Leu	Met	Leu	Val	His	Ser	Arg	Lys	Pro	Gln	Glu	Met	Ile	340	345	350	
Asp	Ile	Trp	Ser	Gln	Leu	Gln	Ser	Ala	His	Leu	Lys	Cys				355	360	365	

<210> 16

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetically generated primer

<400> 16

cttcgacgcc ccacactcat

20

<210> 17

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetically generated primer

<400> 17

atgagtgtgg ggcgtcgaag

20

<210> 18

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetically generated primer

<400> 18

ccatgttggg gtctcacatt agag

24

<210> 19

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetically generated primer

<400> 19

ggtaagtcag accaatatcc tgcc

24